

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/561,292
Source: JFWP
Date Processed by STIC: 01/11/2007

ENTERED



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/561,292

DATE: 01/11/2007

TIME: 09:48:35

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\01112007\J561292.raw

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4 <110> APPLICANT: BOUGUELERET; Lydie
5     CUSIN; Isabelle
7 <120> TITLE OF INVENTION: SECRETED POLYPEPTIDE SPECIES ASSOCIATED
8     WITH CARDIOVASCULAR DISORDERS
11 <130> FILE REFERENCE: DV/4-33628A/GEP US-P
13 <140> CURRENT APPLICATION NUMBER: 10/561,292
14 <141> CURRENT FILING DATE: 2005-12-20
16 <150> PRIOR APPLICATION NUMBER: 60/484,153
17 <151> PRIOR FILING DATE: 2003-06-30
19 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/007047
20 <151> PRIOR FILING DATE: 2004-06-29
22 <160> NUMBER OF SEQ ID NOS: 8
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 456
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: PROPEP
33 <222> LOCATION: (1)...(456)
34 <223> OTHER INFORMATION: Precursor protein of CP22
36 <400> SEQUENCE: 1
37 Met Ile Leu Ser Leu Leu Phe Ser Leu Gly Gly Pro Leu Gly Trp Gly
38 1           5           10           15
39 Leu Leu Gly Ala Trp Ala Gln Ala Ser Ser Thr Ser Leu Ser Asp Leu
40           20           25           30
41 Gln Ser Ser Arg Thr Pro Gly Val Trp Lys Ala Glu Ala Glu Asp Thr
42           35           40           45
43 Gly Lys Asp Pro Val Gly Arg Asn Trp Cys Pro Tyr Pro Met Ser Lys
44           50           55           60
45 Leu Val Thr Leu Leu Ala Leu Cys Lys Thr Glu Lys Phe Leu Ile His
46 65           70           75           80
47 Ser Gln Gln Pro Cys Pro Gln Gly Ala Pro Asp Cys Gln Lys Val Lys
48           85           90           95
49 Val Met Tyr Arg Met Ala His Lys Pro Val Tyr Gln Val Lys Gln Lys
50           100          105          110
51 Val Leu Thr Ser Leu Ala Trp Arg Cys Cys Pro Gly Tyr Thr Gly Pro
52           115          120          125
53 Asn Cys Glu His His Asp Ser Met Ala Ile Pro Glu Pro Ala Asp Pro
54           130          135          140
55 Gly Asp Ser His Gln Glu Pro Gln Asp Gly Pro Val Ser Phe Lys Pro
56 145          150          155          160
57 Gly His Leu Ala Ala Val Ile Asn Glu Val Glu Val Gln Gln Glu Gln

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58          165          170          175
59 Gln Glu His Leu Leu Gly Asp Leu Gln Asn Asp Val His Arg Val Ala
60          180          185          190
61 Asp Ser Leu Pro Gly Leu Trp Lys Ala Leu Pro Gly Asn Leu Thr Ala
62          195          200          205
63 Ala Ser Leu Ser Asn Asp Val Lys Asn Val Gly Arg Cys Cys Glu Ala
64          210          215          220
65 Glu Ala Gly Ala Gly Ala Ala Ser Leu Asn Ala Ser Leu His Gly Leu
66 225          230          235          240
67 His Asn Ala Leu Phe Ala Thr Gln Arg Ser Leu Glu Gln His Gln Arg
68          245          250          255
69 Leu Phe His Ser Leu Phe Gly Asn Phe Gln Gly Leu Met Glu Ala Asn
70          260          265          270
71 Val Ser Leu Asp Leu Gly Lys Leu Gln Thr Met Leu Ser Arg Lys Gly
72          275          280          285
73 Lys Lys Gln Gln Lys Asp Leu Glu Ala Pro Arg Lys Arg Asp Lys Lys
74          290          295          300
75 Glu Ala Glu Pro Leu Val Asp Ile Arg Val Thr Gly Pro Val Pro Gly
76 305          310          315          320
77 Ala Leu Gly Ala Ala Leu Trp Glu Ala Gly Ser Pro Val Ala Phe Tyr
78          325          330          335
79 Ala Ser Phe Ser Glu Gly Thr Ala Ala Leu Gln Thr Val Lys Phe Asn
80          340          345          350
81 Thr Thr Tyr Ile Asn Ile Gly Ser Ser Tyr Phe Pro Glu His Gly Tyr
82          355          360          365
83 Phe Arg Ala Pro Glu Arg Gly Val Tyr Leu Phe Ala Val Ser Val Glu
84          370          375          380
85 Phe Gly Pro Gly Pro Gly Thr Gly Gln Leu Val Phe Gly Gly His His
86 385          390          395          400
87 Arg Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr
88          405          410          415
89 Val Phe Ala Met Ala Glu Leu Gln Lys Gly Glu Arg Val Trp Phe Glu
90          420          425          430
91 Leu Thr Gln Gly Ser Ile Thr Lys Arg Ser Leu Ser Gly Thr Ala Phe
92          435          440          445
93 Gly Gly Phe Leu Met Phe Lys Thr
94          450          455
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 433
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <220> FEATURE:
103 <221> NAME/KEY: PEPTIDE
104 <222> LOCATION: (1)...(433)
105 <223> OTHER INFORMATION: Polypeptide sequence of SEQ ID NO:1 after removal
106 of the signal peptide
108 <400> SEQUENCE: 2
109 Ala Ser Ser Thr Ser Leu Ser Asp Leu Gln Ser Ser Arg Thr Pro Gly
110 1          5          10          15

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111 Val Trp Lys Ala Glu Ala Glu Asp Thr Ser Lys Asp Pro Val Gly Arg
112          20          25          30
113 Asn Trp Cys Pro Tyr Pro Met Ser Lys Leu Val Thr Leu Leu Ala Leu
114          35          40          45
115 Cys Lys Thr Glu Lys Phe Leu Ile His Ser Gln Gln Pro Cys Pro Gln
116          50          55          60
117 Gly Ala Pro Asp Cys Gln Lys Val Lys Val Met Tyr Arg Met Ala His
118 65          70          75          80
119 Lys Pro Val Tyr Gln Val Lys Gln Lys Val Leu Thr Ser Leu Ala Trp
120          85          90          95
121 Arg Cys Cys Pro Gly Tyr Thr Gly Pro Asn Cys Glu His His Asp Ser
122          100         105         110
123 Met Ala Ile Pro Glu Pro Ala Asp Pro Gly Asp Ser His Gln Glu Pro
124          115         120         125
125 Gln Asp Gly Pro Val Ser Phe Lys Pro Gly His Leu Ala Ala Val Ile
126          130         135         140
127 Asn Glu Val Glu Val Gln Gln Glu Gln Glu His Leu Leu Gly Asp
128 145         150         155         160
129 Leu Gln Asn Asp Val His Arg Val Ala Asp Ser Leu Pro Gly Leu Trp
130          165         170         175
131 Lys Ala Leu Pro Gly Asn Leu Thr Ala Ala Ser Leu Ser Asn Asp Val
132          180         185         190
133 Lys Asn Val Gly Arg Cys Cys Glu Ala Glu Ala Gly Ala Gly Ala Ala
134          195         200         205
135 Ser Leu Asn Ala Ser Leu His Gly Leu His Asn Ala Leu Phe Ala Thr
136          210         215         220
137 Gln Arg Ser Leu Glu Gln His Gln Arg Leu Phe His Ser Leu Phe Gly
138 225         230         235         240
139 Asn Phe Gln Gly Leu Met Glu Ala Asn Val Ser Leu Asp Leu Gly Lys
140          245         250         255
141 Leu Gln Thr Met Leu Ser Arg Lys Gly Lys Lys Gln Gln Lys Asp Leu
142          260         265         270
143 Glu Ala Pro Arg Lys Arg Asp Lys Lys Glu Ala Glu Pro Leu Val Asp
144          275         280         285
145 Ile Arg Val Thr Gly Pro Val Pro Gly Ala Leu Gly Ala Ala Leu Trp
146          290         295         300
147 Glu Ala Gly Ser Pro Val Ala Phe Tyr Ala Ser Phe Ser Glu Gly Thr
148 305         310         315         320
149 Ala Ala Leu Gln Thr Val Lys Phe Asn Thr Thr Tyr Ile Asn Ile Gly
150          325         330         335
151 Ser Ser Tyr Phe Pro Glu His Gly Tyr Phe Arg Ala Pro Glu Arg Gly
152          340         345         350
153 Val Tyr Leu Phe Ala Val Ser Val Glu Phe Gly Pro Gly Pro Gly Thr
154          355         360         365
155 Gly Gln Leu Val Phe Gly Gly His His Arg Thr Pro Val Cys Thr Thr
156          370         375         380
157 Gly Gln Gly Ser Gly Ser Thr Ala Thr Val Phe Ala Met Ala Glu Leu
158 385         390         395         400
159 Gln Lys Gly Glu Arg Val Trp Phe Glu Leu Thr Gln Gly Ser Ile Thr

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160                               405                               410                               415
161 Lys Arg Ser Leu Ser Gly Thr Ala Phe Gly Gly Phe Leu Met Phe Lys
162                               420                               425                               430
163 Thr
167 <210> SEQ ID NO: 3
168 <211> LENGTH: 152
169 <212> TYPE: PRT
170 <213> ORGANISM: Homo sapiens
172 <220> FEATURE:
173 <221> NAME/KEY: PEPTIDE
174 <222> LOCATION: (1)...(152)
175 <223> OTHER INFORMATION: Cardiovascular disorder Plasma Polypeptide 22 (CPP
176 22)
178 <400> SEQUENCE: 3
179 Glu Ala Glu Pro Leu Val Asp Ile Arg Val Thr Gly Pro Val Pro Gly
180 1 5 10 15
181 Ala Leu Gly Ala Ala Leu Trp Glu Ala Gly Ser Pro Val Ala Phe Tyr
182 20 25 30
183 Ala Ser Phe Ser Glu Gly Thr Ala Ala Leu Gln Thr Val Lys Phe Asn
184 35 40 45
185 Thr Thr Tyr Ile Asn Ile Gly Ser Ser Tyr Phe Pro Glu His Gly Tyr
186 50 55 60
187 Phe Arg Ala Pro Glu Arg Gly Val Tyr Leu Phe Ala Val Ser Val Glu
188 65 70 75 80
189 Phe Gly Pro Gly Pro Gly Thr Gly Gln Leu Val Phe Gly Gly His His
190 85 90 95
191 Arg Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr
192 100 105 110
193 Val Phe Ala Met Ala Glu Leu Gln Lys Gly Glu Arg Val Trp Phe Glu
194 115 120 125
195 Leu Thr Gln Gly Ser Ile Thr Lys Arg Ser Leu Ser Gly Thr Ala Phe
196 130 135 140
197 Gly Gly Phe Leu Met Phe Lys Thr
198 145 150
201 <210> SEQ ID NO: 4
202 <211> LENGTH: 24
203 <212> TYPE: PRT
204 <213> ORGANISM: Homo sapiens
206 <220> FEATURE:
207 <221> NAME/KEY: PEPTIDE
208 <222> LOCATION: (1)...(24)
209 <223> OTHER INFORMATION: Tryptic peptides of CPP 22 found by MS-MS mass
210 spectrometry in plasma samples of individuals with
211 coronary artery disease
213 <400> SEQUENCE: 4
214 Thr Pro Val Cys Thr Thr Gly Gln Gly Ser Gly Ser Thr Ala Thr Val
215 1 5 10 15
216 Phe Ala Met Ala Glu Leu Gln Lys
217 20

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220 <210> SEQ ID NO: 5
221 <211> LENGTH: 12
222 <212> TYPE: PRT
223 <213> ORGANISM: Homo sapiens
225 <220> FEATURE:
226 <221> NAME/KEY: PEPTIDE
227 <222> LOCATION: (1)...(12)
228 <223> OTHER INFORMATION: Tryptic peptides of CPP 22 found by MS-MS mass
229     spectrometry in plasma samples of individuals with
230     coronary artery disease
232 <400> SEQUENCE: 5
233 Val Trp Phe Glu Leu Thr Gln Gly Ser Ile Thr Lys
234 1      5      10
237 <210> SEQ ID NO: 6
238 <211> LENGTH: 14
239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
242 <220> FEATURE:
243 <221> NAME/KEY: PEPTIDE
244 <222> LOCATION: (1)...(14)
245 <223> OTHER INFORMATION: Tryptic peptides of CPP 22 found by MS-MS mass
246     spectrometry in plasma samples of individuals with
247     coronary artery disease
249 <400> SEQUENCE: 6
250 Ser Leu Ser Gly Thr Ala Phe Gly Gly Phe Leu Met Phe Lys
251 1      5      10
254 <210> SEQ ID NO: 7
255 <211> LENGTH: 1371
256 <212> TYPE: DNA
257 <213> ORGANISM: Homo sapiens
259 <220> FEATURE:
260 <221> NAME/KEY: variation
261 <222> LOCATION: (1)...(1371)
262 <223> OTHER INFORMATION: Splice variant of the Endoglyx-1 gene and
263     comprises the cDNA coding sequence for SEQ ID NO:
264     1
266 <400> SEQUENCE: 7
267 atgacacctga gcttgctgtt cagccttggg ggccccctgg gctgggggct gctgggggca 60
268 tgggccagg cttccagtag tagcctctct gatctgcaga gctccaggac acctgggggtc 120
269 tggaaggcag aggctgagga caccggcaag gaccccgtag gacgtaactg gtgcccctac 180
270 ccaatgtcca agctggtcac cttactagct ctttgcaaaa cagagaaatt cctcatccac 240
271 tcgcagcagc cgtgtccgca gggagctcca gactgccaga aagtcaaagt catgtaccgc 300
272 atggcccaca agccagtgtg ccagggtcaag cagaagggtg tgacctcttt ggctggagg 360
273 tgctgccctg gctacacggg cccaactgc gagcaccacg attccatggc aatccctgag 420
274 cctgcagatc ctggtgacag ccaccaggaa cctcaggatg gaccagtcag cttcaaacct 480
275 ggccaccttg ctgcagtgat caatgaggtt gaggtgcaac aggaacagca ggaacatctg 540
276 ctggggagatc tccagaatga tgtgcaccgg gtggcagaca gcctgccagg cctgtggaaa 600
277 gccctgacctg gtaacctcac agctgcaagc ctgagcaacg acgtcaagaa tgtcgggcgg 660
278 tgctgcgagg ccgaggccgg ggccggggcc gcctccctca acgcctccct tcacggcctc 720

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VERIFICATION SUMMARY

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